

#6



PCT09

## RAW SEQUENCE LISTING

DATE: 06/06/2002

PATENT APPLICATION: US/09/869,540A

TIME: 12:47:09

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3 <110> APPLICANT: MORI, MASAOKI  
 4 SHIMOMURA, YUKIO  
 5 TAKEKAWA, SHIRO  
 6 SUGO, TSUKASA  
 7 ISHIBASHI, YOSHIHIRO  
 8 KITADA, CHIEKO  
 9 SUZUKI, NOBUHIRO  
 11 <120> TITLE OF INVENTION: SCREENING METHOD  
 13 <130> FILE REFERENCE: 56001(46342)  
 15 <140> CURRENT APPLICATION NUMBER: 09/869,540A  
 16 <141> CURRENT FILING DATE: 2001-11-23  
 18 <150> PRIOR APPLICATION NUMBER: PCT/JP99/07337  
 19 <151> PRIOR FILING DATE: 1999-12-27  
 21 <150> PRIOR APPLICATION NUMBER: JP 10-374454  
 22 <151> PRIOR FILING DATE: 1998-12-28  
 24 <150> PRIOR APPLICATION NUMBER: JP 11-122688  
 25 <151> PRIOR FILING DATE: 1999-04-28  
 27 <150> PRIOR APPLICATION NUMBER: JP 11-249300  
 28 <151> PRIOR FILING DATE: 1999-09-02  
 30 <160> NUMBER OF SEQ ID NOS: 24  
 32 <170> SOFTWARE: PatentIn Ver. 2.1  
 34 <210> SEQ ID NO: 1  
 35 <211> LENGTH: 16  
 36 <212> TYPE: PRT  
 37 <213> ORGANISM: Rattus sp.  
 39 <220> FEATURE:  
 40 <223> OTHER INFORMATION: The 7th cysteine residue binds with the 16th cysteine  
 41 residue to form a intra-molecular disulfide-bond  
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 44 Asp Phe Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys  
 45 1 5 10 15  
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 55 residue to form a intra-molecular disulfide-bond  
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 58 Asp Phe Asp Met Leu Arg Cys Met Leu Gly Arg Val Tyr Arg Pro Cys  
 59 1 5 10 15  
 61 Trp Gln Val  
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101           20           25           30
103 Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
104           35           40           45
106 Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
107           50           55           60
109 Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
110           65           70           75           80
112 Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
113           85           90           95
115 Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
116           100          105          110
118 Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
119           115          120          125
121 Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala
122           130          135          140
124 Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala
125 145           150           155           160
127 Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
128           165           170           175
130 Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
131           180           185           190
133 Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
134           195           200           205
136 Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile

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139 Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala
140 225      230      235      240
142 Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
143      245      250      255
145 Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
146      260      265      270
148 Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
149      275      280      285
151 Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
152      290      295      300
154 Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
155 305      310      315      320
157 Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr
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160 Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
161      340      345      350
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175 atcaacatca ttatgccttc cgtgttttgt accatctgtc tcctgggcat cgtgggaaac 180
176 tccacggtca tctttgtgtg ggtgaagaag tccaagctac actggtgcag caacgtcccc 240
177 gacatcttca tcatcaacct ctctgtgtgt gatctgtctt tcctgctggg catgcctttc 300
178 atgatccacc agtcatggg gaacggcgtc tggcactttg gggaaaccat gtgcaccctc 360
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200 uccugcagcc cgggggaucc gccacuagu ucaggugccu uugcuuucug uccucuccuc 120
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226     oligonucleotide
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239 ggcagcggtc gccaggctac ggaggaagac ccccttccca actgcggggc ttgcgctccg 120
240 ggacaagggtg gcaggcgctg gaggtgcccg cagcctgcgt ggggtggaggg gagctcagct 180
241 cggttgtggg agcaggcgac cggcactggc tggatggacc tggaaagctc gctgctgccc 240
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263 <211> LENGTH: 422

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275 35 40 45
277 Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
278 50 55 60
280 Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
281 65 70 75 80
283 Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
284 85 90 95
286 Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
287 100 105 110
289 Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
290 115 120 125
292 Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
293 130 135 140
295 Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
296 145 150 155 160
298 Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
299 165 170 175
301 Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
302 180 185 190
304 Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
305 195 200 205
307 Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
308 210 215 220
310 Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
311 225 230 235 240
313 Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
314 245 250 255
316 Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
317 260 265 270
319 Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
320 275 280 285
322 Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
323 290 295 300
325 Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
326 305 310 315 320
328 Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
329 325 330 335
331 Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
332 340 345 350
334 Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
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VERIFICATION SUMMARY

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